

Static Sequence Search Report 17A-

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GenCore version 4.5  
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## Om nucleic - nucleic search, using sw model

Run on:

April 3, 2000, 03:22:17 ; Search time 528.89 Seconds  
(without alignments)  
-6028.103 Million cell updates/sec

Title: US-09-459-774-1

Perfect score: 1050  
Sequence: 1 atgaaaccggaaagcgccggc.....agatgtacacgtgcagaatgtga 1050

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 821193 seqs, - 1518192014 residues

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Database : Listing first 45 summaries

1: GenEmbl:  
2: gb\_bal:  
3: gb\_cm:  
4: gb\_cv:  
5: gb\_pat:  
6: gb\_ph:  
7: gb\_ppl:  
8: gb\_pl2:  
9: gb\_pr1:  
10: gb\_pr2:  
11: gb\_pr3:  
12: gb\_ro:  
13: gb\_sts:  
14: gb\_sy:  
15: gb\_un:  
16: gb\_vl:  
17: em\_fun:  
18: em\_hun1:  
19: em\_hun2:  
20: em\_in:  
21: em\_cm:  
22: em\_cv:  
23: em\_cv:  
24: em\_pat:  
25: em\_ph:  
26: em\_pl:  
27: em\_ro:  
28: em\_sts:  
29: em\_sy:  
30: em\_un:  
31: em\_vl:  
32: gb\_hq1:  
33: gb\_hq2:  
34: gb\_in1:  
35: gb\_in2:  
36: em\_bal:  
37: em\_ba2:  
38: em\_hun3:  
39: em\_hun4:  
40: gb\_pr:  
41: gb\_htc3:  
42: gb\_htc4:  
43: gb\_htc5:  
44: gb\_jtg6:  
45: gb\_htc7:  
46: em\_htc1:  
47: em\_htc2:  
48: em\_hq3:  
49: em\_hun5:  
50: gb\_p13:  
1: D83175 LOCUS D83175 1442 DP mRNA  
DEFINITION Homo sapiens WNT7a mRNA, complete cds.  
ACCESSION D83175  
VERSION D83175.1 GI:5509900  
KEYWORDS WNT7a.

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1045.2	99.5	1442 9 D83175	D83175 Homo sapien
2	1038.8	98.9	11 HSU53476	HSU53476 Human proto
3	926.8	88.3	1050 12 MUSWNT7A	M89801 Mouse Wnt-7
4	678.8	64.6	1449 12 MUSWNT7B	M89802 Mouse Wnt-7
5	675.6	64.3	1948 4 PWT80581	U80581 Pleurodeles
6	586	55.8	1199 4 AF026894	AF026894 Xenopus 1
7	482.2	45.9	245767 42 AC011607	AC011607 Homo sapi
8	479.9	45.7	42 AC011607	AF061975 Homo sapi
9	297.4	28.3	1427 4 CHXW4P	CHXW4P Chicken mRNA
10	292.6	27.9	1292 4 AF182403	AF182403 Gallus ga
11	275	26.2	245767 42 AC011607	AC011607 Homo sapi
12	283	27.0	1101 12 MUSWNT7A	AF188608 Rat
13	283	27.0	1252 34 DMWNT2NR	M89977 Mouse Wnt-4
14	283	27.0	1500 12 AF070988	AF070988 Mus muscu
15	275.8	26.4	3000 12 MUSINT4	M82502 Mouse proto
16	275	26.2	245767 42 AC011607	AC011607 Homo sapi
17	272.8	26.0	4114 12 MUSWNT7A	AF188608 Rat
18	261.2	24.9	2385 9 HSWNT13	M89977 Mouse Wnt-4
19	254.6	24.2	2664 4 AMWNT5B	X64735 D.melanogas
20	252.2	24.0	369 4 PLETH7A	AF070988 Mus muscu
21	248.8	23.7	1523 12 MUSINT4	M82502 Mouse proto
22	248.8	23.7	1690 12 MUSWNT7A	AF070988 Rat
23	248.8	23.7	1980 9 AF188333	AF188333 Homo sapiens
24	245.2	23.4	3056 35 AF051973	AF051973 Branchios
25	244	23.2	1509 4 DRUS1266	Z14048 A.mexicanum
26	243.2	23.2	4 GOOR7A	M81295 Pletiodon j
27	241.6	23.0	369 4 TKYWNT7A	M89799 Mouse Wnt-5
28	241	23.0	1059 4 AF051541	M89798 Mouse Wnt-5
29	240.2	22.9	2230 12 MUSWNT7A	X56842 Mouse mRNA
30	236	22.5	372 4 XELANT7A	L07533 Xenopus lae
31	235.6	22.4	2301 9 HSIRP	X78786 Human mRNA
32	235	22.4	1943 4 AB006014	AB006014 Danio rerio
33	234.8	22.4	2076 35 SP058982	M91261 Chen caerule
34	234.6	22.3	1778 4 DRUS1267	M91261 Danio rerio
35	233.4	22.2	2230 12 MUSINT4	US21267 Danio rerio
36	233.2	22.2	1372 5 AR018070	M11943 Mouse int-1
37	226	21.5	3574 4 AMWNT5A	AR018070 Sequence
38	224.6	21.4	4 AB024080	Z14047 A.mexicanum
39	223.2	21.3	1160 4 PWT80581	AB024080 Gallus ga
40	219.6	20.9	1170 4 PWT80582	U80582 Pleurodeles
41	219.4	20.9	1188 4 XLWNT5C	US1268 Danio rerio
42	218.6	20.8	369 4 EPWT7T	X73510 X.leavis
43	210.6	20.1	369 4 AOPWNT7A	M91269 Eptatretus
44	210.4	20.0	372 4 XEWNT7B	M91256 Alopas vul
45	20.0	2372 35 AF061974	L07534 Xenopus lae	

## ALIGNMENTS

RESULT 1  
D83175 LOCUS D83175 1442 DP mRNA  
DEFINITION Homo sapiens WNT7a mRNA, complete cds.  
ACCESSION D83175  
VERSION D83175.1 GI:5509900  
KEYWORDS WNT7a.

PRI

16-JUL-1999



























Mon Apr 3 09:45:58 2000

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Qy 827 actactggaggaggaccggtaacccggcagtgtggaccaccaggcgccgcgtcaaca 886  
Db 890 ACTTTGTCAGCCAAACCCAGAGGGGCTCCTTGGTACCGACGGACTTGCAATG 949  
Qy 887 agacggctccacggccggctgtgacctcaatgtctgtgtgggggttacacaccc 946  
Db 950 TCACCTCCACGCCATGATGGCTGGATCTGCTGCTGCTGGGGGCCACACAGA 1009  
Qy 947 accggtaacggccgggtggcactgtcaatgtttcaatgtgtgtgtatgtcaagt 1006  
Db 1010 GGACGGAGAACGGAGGAATGCCATTGCCATGCCACTGTGCCTATGTCAGCT 1069  
Qy 1007 gcacacatgcacggagggcacggagaatgttacggtgaagt 1048  
Db 1070 GCCAAGAGTGATTCGCATCTACCATGTCACACTGCAAGT 1111

Search completed: April 3, 2000, 04:12:53  
Time: 3036 sec

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QY	121	ACTCGNLISDCGCDKERQGHRDEGKWRGGCSADIRYIGIGFAKVFDAREIKONARTLM	PRELIMINARY;	PRT;	349 AA.
AC	0042258				
Db	181	NLHNNEAGRKLLEENMKLECKCHGVGSCTTKTCWTLPLQRELGVLKDKNAYHEPV	04-2258; DT 01-JUN-1998 (TREMBlr. 05, Created)		
QY	181	NLHNNEAGRKLLEENMKLECKCHGVGSCTTKTCWTLPLQRELGVLKDKNAYHEPV	DT 01-JAN-1998 (TREMBlr. 05, Last sequence update)		
Db	241	VRASNRKRPTELIKIKPLSYKPMDDLVYERSPVCEDVTGSGVQGRACNTAQ	DT 01-NOV-1999 (TREMBlr. 12, Last annotation update)		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	DE WNT7B.		
Db	241	VRASNRKRPTELIKIKPLSYKPMDDLVYERSPVCEDVTGSGVQGRACNTAQ	GN XNNT7B.		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	349		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	Xenopus laevis (African clawed frog).		
OC			Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;		
OC			Xenopus.		
RN	[1]	SEQUENCE FROM N.A.			
RA	CHANG C., HEMMATI-BRIVANLOU A.				
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.				
CC	-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.				
DR	EMBL: AF028894; RAB8275.1; -.				
DR	PROSITE: PS00246; WNT1; 1.				
DR	PPM; PF00110; wnt; 1.				
KW	Developmental protein; Glycoprotein.				
RN	SEQUENCE	349 AA; 39740 MW; B66604B5 CRC32;			
RA	SEQUENCE FROM N.A.				
RA	CAUBIT X., NICOLAS S., LE PARCO Y.;				
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.				
CC	-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.				
DR	EMBL; U80891; AA858474.1; -.				
DR	PROSITE: PS00246; WNT1; 1.				
DR	PFAM; PF00110; wnt; 1.				
KW	Pfam; Protein; Glycoprotein.				
SQ	SEQUENCE	348 AA; 39039 MW; 5F951309 CRC32;			
Query Match					
Best Local Similarity	89.7%	Score 2387; DB 13; Length 348;			
Matches	87.4%	Pred. No. 0.00e+00;			
Matches	305;	Conservative 30; Mismatches 13; Indels 1; Gaps 1;			
Db	1	MNKKTRRWIFHFLSLGIVYTKIGGSSVVALGASTICNRIPGLAPRORTICQNRPDAI	01 AUG 1998 (TREMBlr. 07, Created)		
QY	1	MNKKTRRWIFHFLSLGIVYTKIGGSSVVALGASTICNRIPGLAPRORTICQNRPDAI	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
Db	61	IIGEGROMGNEQCYQPERIGRWNCSALGERIVFGQDLRVGSREAATYAITAGVHA	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
QY	61	IIGEGROMGNEQCYQPERIGRWNCSALGERIVFGQDLRVGSREAATYAITAGVHA	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
Db	121	SACSGQNLNSGCCDKEQKQYNOEGKWWGCSADIRYIGIDFSRKFDAREIKNARRLM	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
QY	121	SACSGQNLNSGCCDKEQKQYNOEGKWWGCSADIRYIGIDFSRKFDAREIKNARRLM	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
Db	181	NLHNNEAGRKLLEENMKLECKCHGVGSCTTKTCWTLPLQRELGVLKDKNAYHEPV	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
QY	181	NLHNNEAGRKLLEENMKLECKCHGVGSCTTKTCWTLPLQRELGVLKDKNAYHEPV	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
Db	241	VRASNRKRPTELIKIKPLSYKPMDDLVYERSPVCEDVTGSGVQGRACNTAQ	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
QY	241	VRASNRKRPTELIKIKPLSYKPMDDLVYERSPVCEDVTGSGVQGRACNTAQ	01-AUG-1998 (TREMBlr. 07, Last sequence update)		
Db	301	TGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	DE WNT7B.		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	GN XNNT7B.		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	Branchiostoma floridae (Florida lancelet) (Amphioxus); Branchiostomidae; Branchiostoma.		
QY	301	ASGCDLMCCGCGYNTHOARYWOCNCFKHMCYVKNTCSERTEMTICK	Branchiostoma; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.		
RN	[1]	SEQUENCE FROM N.A.			
RA	SCHUBERT M., HOLLAND L. Z., JACOBS D. K., HOLLAND N. D.;				
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING				

CC	MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).	Db	63 SEVITIAGOLPCSLAGUSQOKKLQJYQDHMFFIGEAKIGIKEOYQFRHRWCST 122
CC	-!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.	Qy	27 SSVALGASLICINCKIPGLAPRQRACIQSRPDAIVIGGSQMLDEQFORNGRNCSA 86
CC	-!- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.	Db	123 VDNNSVFGRMQTSRETAFTYAVSAAGVNNMSRACREGELSSCGGSRAIRPKDLPRD- 181
DR	EMBL; AF061975; AAC80433.1; -.	Qy	87 LGERTVFGKELVGSRERAFPTIAAGVHAITAECTQGNLSDCGDK-E-KOGOYHRDE 145
DR	PROSITE: PS00246; WNT1; 1.	Db	182 -WLMGGCGNIEGYRFKEFEVARDERRVYQNGSISARMIMLNHNEAGRRTVYNAD 240
KW	Developmental protein.	Qy	QY 146 GWKNGCSDAIRYGIFAKFVDARE--I-K---QNARTLMNLHNEAGRKILEENMK 197
SQ	SEQUENCE 347 AA; 39425 MW; CF2DAAGE CRC32;	Db	241 VACKCHGVSGSCSIKTCWQLADFRKGDKKDYKDSAAK-M-L-NSRK---L-VQMN 293
Db	8 RYKAV-LCVA-I-LQLESLSTVVALGANICNICNIPGLYPRORACIQTRPDLVIAIGSA 64	Qy	198 LECKCHGVSGSCSIKTCWMLPQFRELGYVLUKYOKVYNEAVHVEVYRASENKRPTFLKIKP 257
Db	7 RCGLCHFLISLGVMVLRIGGFSSVVAlAGASILCNCNIPGLAPRORACIQSRPDAIVIGES 66	Db	294 SRFNAPTIHDILYIDPSDYMCRMNESTSGLTGRLCNKTSEGNDGCILMCCGRGYQDFK 353
Db	65 ORGDECRCQFRHSRWNCGMNDNUNFGELRGSKEARFTYASSALVHATVACQG 124	Qy	258 LSVKPKMDTDLWIEKSPNCEEDPVGSVGTGRCACKTAPASGCDIMCCGORGYNTQ 317
Qy	67 QMGIDECQFQRNRWRNCALGERTVEKGELKVSKREAFTYATAAGVHAITAQCTQG 126	Db	354 TVDERSCHCKFHCCYVICKLCPEIVDOPVCK 385
Db	125 NISDCGCDRTKEGDLN-DEGWKNGCSCADVYKGRFKKFVDAREVEQARALMNHLHNE 183	Qy	QY 318 YARVWQNCCKFHCCYVICKCNCBSERTEMYTC 349
Qy	127 NLSCCGCDEKEQSYHRCGKQHGSADIRYKGRFKFVDAREIKARNLHNNE 186	RESULT	RESULT 6
Db	184 AGRVIDQHTRBLECKCHGVSGSCMKTCWITLPREFREVNILKRYHDAQLYAVARR 243	ID	096867
Qy	187 AGRKILEENMKLEKCHGVSGSCMKTCWITLPREFREVNILKRYHDAQLYAVARR 245	PRELIMINARY;	PRELIMINARY;
Db	244 TRRFLFLKNSRPFKEPREISUYLRLSPNYCERDEATSLTGRGRNRTFPYDGED 303	PRT;	PRT; 331 AA.
Qy	246 NKRTPFLKIKPLSYRKPMTDLTVIERSPNCEEDPVGSVGTGRCACKTAPASGCD 305	DT	01-MAY-1999 (TREMBlrel. 10, Created)
Db	304 LMCGGGRGYWTHQFWKTWQNCNCFHWCCYVCKCNCQNSERTEYTC 347	DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)
Qy	305 LMCGGGRGYWTHQFWQNCNCFHWCCYVCKCNCQNSERTEYTC 349	DE	01-NOV-1999 (TREMBlrel. 12, Last annotation update)
RP	SEQUENCE FROM N.A.	GN	DELL SIGNALING MOLECULE WNT-5 (FRAGMENT).
RX	RX MEDLINE; 98320538.	SPWNT-5;	Strongylocentrotus purpuratus (Purple sea urchin).
RA	RA FERKOWICZ,M.J., STANDER M.C., RAFF R.A.;	OS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrates; Archosuria; Aves; Euchinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
RT	RT "Phylogenetic relationships and developmental expression of three sea urchin Wnt genes."	OS	[1]
DT	DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)	OC	Medline; 98320538.
DT	DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)	OC	RT
DT	DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)	OC	RT
DT	DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)	OC	RT
OS	OS Gallus gallus (Chicken).	CC	CC
OS	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Archosuria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.	CC	CC
OS	OS SEQUENCE FROM N.A.	CC	CC
OS	OS TISSUE-EMBRYO; MEDLINE; 9932672.	CC	CC
OS	OS KAWAKAMI, Y.; WADA, N.; NISHIMATSU, S.; ISHIKAWA, T.; NOJI, S.; NOHNO, T.;	CC	CC
OS	OS "Involvement of Wnt-5a in chondrogenic pattern formation in the chick limb bud," Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).	CC	CC
OS	OS "Involvement of Wnt-5a in chondrogenic pattern formation in the chick limb bud," Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).	CC	CC
OS	OS "Involvement of Wnt-5a in chondrogenic pattern formation in the chick limb bud," Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS Dev. Growth Differ. 41:29-40(1999).	CC	CC
OS	OS -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.	CC	CC
OS	OS -!- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.	CC	CC
DR	DR EMBL; AB0604; BAA75242.1; -.	CC	CC
DR	DR PROSITE: PS00246; WNT1; 1.	CC	CC
KW	KW Developmental protein; Glycoprotein.	CC	CC
SQ	SQ SEQUENCE 385 AA; 43005 MW; IC8EA6D9 CRC32;	FT	14 LGTOPLCSEBLIGLSPGQOKLQYQDHMAPISGAKMSIDECONQTNRWNCSTVDNN 73
Query Match	Query Match 40.8%; Score 1085; DB 5; Length 331; Best Local Similarity 50.2%; Pred. No. 5.69e-262; Matches 164; Conservative 53; Mismatches 92; Indels 18; Gaps 10;	Qy	32 LGASICNCKIPGLAPRORACIQSRPDAIVIGEGSQMLDECQFRNGRNCSA 91
Best Local Similarity	Best Local Similarity 47.3%; Pred. No. 4.33e-265; Score 1097; DB 13; Length 385;	Db	74 VFGKLSTSSREAFAYTASAGVNNMSRACREGELSSCGGSRAIRPKDLPRD- 131
Best Local Similarity	Best Local Similarity 47.3%; Pred. No. 4.33e-265; Score 1097; DB 13; Length 385;	Qy	92 VFGKLVSKREAFTYAIIAGVWAHTACTQGNLSDCGDK-E-KOGOYHRDEGRKG 150
Best Local Similarity	Best Local Similarity 47.3%; Pred. No. 4.33e-265; Score 1097; DB 13; Length 385;	Db	132 GCGNIDGFREFEVDFARERMENPQGSEFYDMMNLHNEAGKAVYDAGTCK 191

OY	151	GCSADIRYIGFAKVFUDARIKQNA-R--T--L-MNHNNNEAGRKILENNMLECKC	202	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;				
Db	192	HGVSGSCSLKTCWLOLSPENRUGTILKRDKGATVY--RV--NRKGR-L-VNSDARENK	244	OC	Tetrapodiformes; Tetradontoidei; Tetraodontidae; Fugu;				
OY	203	HGVSGSCTTKTCWTLPOFRELGYVLKDKNNEAVHVEPVRAKRASKRNKRPTFLIKPLSYRK	262	[1]	SEQUENCE FROM N.A.				
Db	245	PTRDILVLYQPSPDYCLPDTGSGTGTGRCNKSMGTPGCTACCGROYNSTKEVVE	304	RA	GELLNER K.; BRENNER S.; GELLNER, K.; BRENNER, S.;				
OY	263	PMDTBLYIEKSPNYCEEDPVYSGTQGRACKTAPQASGCDLMCCGROGYNTHQARYVN	322	RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.				
Db	305	RCKCKERKWCYCVKCRKORTLVDHVH	331	CC	-I- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY				
OY	323	QCNCRPHWCCIVVKCNCSERTEMYICK	349	CC	-I- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.				
RESULT	7	PRELIMINARY;	PRT;	361 AA.	CC	-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.			
ID	O9Y5CO				CC	-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.			
AC	O9Y5CO;				CC	-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.			
DT	01-NOV-1999	(T-EMBLrel. 12, Created)			DR	EMBL: AF056116; AAC34388; 1; -.			
DT	01-NOV-1999	(T-EMBLrel. 12, Last sequence update)			DR	PROSITE: PS00246; WNT1; 1.			
DT	01-NOV-1999	(T-EMBLrel. 12, Last annotation update)			DR	PFAM: PF00110; wnt; 1.			
OS		WNT16 PROTEIN.			KW	Developmental protein; Glycoprotein.			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia;			DR	EMBL: AF056116; AAC34388; 1; -.			
OC		Butterlia; Primates; Catarrhini; Homidae; Homo.			DR	PROSITE: PS00246; WNT1; 1.			
RP		[1]			DR	PFAM: PF00110; wnt; 1.			
RP		SEQUENCE FROM N.A.			DR	EMBL: AF056116; AAC34388; 1; -.			
RC		TISSUE-PLACENTA;			DR	PROSITE: PS00246; WNT1; 1.			
RA		BARNES M.R., KELSELL D.P., FEAR M.W.,			DR	PFAM: PF00110; wnt; 1.			
RT		"Cloning and characterization of human Wnt16, a novel member of the Wnt gene family.",			DR	EMBL: AF056116; AAC34388; 1; -.			
RT		Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.			DR	PROSITE: PS00246; WNT1; 1.			
DR		EMBL: AF152584; AAP08052; 1; -.			DR	PFAM: PF00110; wnt; 1.			
SQ		SEQUENCE 361 AA; 40558 MW; D59A8ED6 CRC32;			DR	EMBL: AF056116; AAC34388; 1; -.			
Query Match	39.1%	Score 1040; DB 4; Length 361;			DR	PROSITE: PS00246; WNT1; 1.			
Best Local Similarity	44.6%	Score 1040; DB 4; Length 361;			DR	PFAM: PF00110; wnt; 1.			
Matches	145;	Conservative			DR	EMBL: AF056116; AAC34388; 1; -.			
Matches	145;	Conservative			DR	PROSITE: PS00246; WNT1; 1.			
Matches	145;	Conservative			DR	PFAM: PF00110; wnt; 1.			
Db	43	CANLP-LNSRKELCKRKPPILPSIREGARLGICQCRSRHERNCMTAAATAPMGA	101	QY	44	LAPRORACOSRPRATIVIGEFSGMGLDPCOFQFRNGRNWNSALGERTVFGKLKVSE	103		
OY	38	CNKKIGLAPRORATIQSRPDAIVITGEVSQNGLSDCGCFOFQRNGRNWNSALGERTVFGKLKVSE	101	Db	123	TAFFPAIMAGVTHAVARSSEGAEIFCTCDYERRGP--GGPDWKHGCGSDNVEGRMFS	180		
Db	102	SPLFGVELSSCTKETAFIYAVMAAGLVHSVTRCSAGNMTECSCDNTLQNGGSASEGWHW	161	QY	104	AAFTYAITAGVHAITAATCTQGNSLSDGDKSKQGQYHRDDESWKKGCSADIRYIGFA	163		
OY	90	RTVFGKELKVSREAFTYIAIAGVVAHTACTQGNLSDCGCKEKOCQYHROEGWKN	149	Db	181	REFVDSSEGRDRLVLTNHNNEAGRMTVSSEMREOECRGHMGSGCATVRTCWNLRLPSRM	240		
Db	162	GGCSDDPVQGMWSRFKSFELDFPIGNTTGKRNVLMLNNHEAGQAVAKLMSVDCRCHG	221	QY	164	KVFDAREIKQNARTLMNLNNNEAGRKILENNMLECKCHGVSQSCITKTCWTLPOFRE	223		
OY	150	GGCSADIRYIGFARKFVD-AR-EIK-QNARTL--MNLHNNEAGRKILENNMLECKCHG	204	Db	241	VGDELKDREDGASRVYVAKGSNRASHRAPHRLPEP-P-AKRPSSMDLYFEKSPNFC	299		
Db	222	VSGSCAVKTGKMTMSFEKKGHLKDYKQNSIQID-KIRKMRKR-EKQPKRHK-	277	QY	224	IGYVLRKDVNEAVIVE-PVRS-R-NKR--PTFLKIKPLSYRKPMDDLVTEKSPNC	278		
OY	205	VSGSCAVKTGKMTPSFEKKGHLKDYKQNSIQID-KIRKMRKR-EKQPKRHK-	277	Db	300	SYSGKGTGTTGSGRACNSTSPGLGDCCELLCCGCFKIRTESMTERCHTFHWCHVSCLN	359		
Db	278	D-DLLVNVKSPNYCVEDKKLGIPPTGQREGNRTSEGADGENLLOGRGYVTHVVRVERC	336	QY	279	EEDPVYSGTQGRACKTAPQASGCDLMCCGROGYNTHQARYWQNCFKHGCCVYKNT	338		
OY	265	DTDLVYIEKSPNYCEDPVYSGTQGRACKTAPQASGCDLMCCGROGYNTHQARYWQNC	324	Db	360	CTSTRILHOC	369		
Db	337	ECKFTWCCYVRCRRESMVTWCK	361	QY	339	CSERTEMYC	348		
OY	325	NCKFHMCYCVCNTCSERTEMYCK	349	RESULT	9	PRELIMINARY;	PRT;	252 AA.	
RESULT	8	PRELIMINARY;	PRT;	370 AA.	ID	P9151;	PRELIMINARY;	PRT;	252 AA.
ID	P79752				AC	P9151;	PRELIMINARY;	PRT;	252 AA.
AC	P79752;				DT	01-MAY-1997	(TREMBrel. 03, Created)		
DT	01-MAY-1997	(TREMBrel. 03, Last sequence update)			DT	01-MAY-1997	(TREMBrel. 03, Last sequence update)		
DT	01-MAY-1997	(TREMBrel. 03, Last annotation update)			DT	01-NOV-1999	(TREMBrel. 12, Last annotation update)		
DE	WNT1.				DE	WNT-4 PROTEIN (FRAGMENT).			
OS		Helicocidaris erythrogramma (Sea urchin).			DN	HEWNT-4.			
OC		Eukaryota; Metazoa; Echinodermata; Echinocozoa; Echinoidea; Echinolamellida; Echinocephala; Echinochela; Echinochelida; Helicocidaris.			DR	EMBL: U88626; AAC59242; 1; -.			
OC		SEQUENCE FROM N.A.			DR	PROSITE: PS00246; WNT1; 1.			
OC		J. MOL. EVOL. 0:0-0(0).			DR	PFAM: PF00110; wnt; 1.			
CC		FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY			DR	EMBL: AF056116; AAC34388; 1; -.			
CC		SIMILARITY).			DR	PROSITE: PS00246; WNT1; 1.			
CC		EXTRACELLULAR MATRIX.			DR	PFAM: PF00110; wnt; 1.			
CC		-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.			DR	EMBL: AF056116; AAC34388; 1; -.			
CC		SEQUENCE FROM N.A.			DR	PROSITE: PS00246; WNT1; 1.			
CC		FERKOWICZ M.J., STANDER M.C., RAFF R.A.;			DR	PFAM: PF00110; wnt; 1.			
CC		SEQUENCE FROM N.A.			DR	EMBL: AF056116; AAC34388; 1; -.			
CC		J. MOL. EVOL. 0:0-0(0).			DR	PROSITE: PS00246; WNT1; 1.			
CC		FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY			DR	EMBL: AF056116; AAC34388; 1; -.			
CC		SIMILARITY).			DR	PROSITE: PS00246; WNT1; 1.			
CC		EXTRACELLULAR MATRIX.			DR	PFAM: PF00110; wnt; 1.			
CC		-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.			DR	EMBL: AF056116; AAC34388; 1; -.			
CC		SEQUENCE FROM N.A.			DR	PROSITE: PS00246; WNT1; 1.			
CC		Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			DR	PFAM: PF00110; wnt; 1.			



QY	309	CGLMCCGCGYNAYTEVLYERCOCKYHNCVYSSCKTCKRTVERVVK	354	244	SRNKRPFLKIKPLSLTRKPMOTDLYIEKSNSNYCEDPPVGSVGTGRACKTAQASG	303
DB	304	CDLMCCGCGYNTQYARWQNCCKFHNCVYVNCNTCSERTEMTCK	349	RP	SEQUENCE FROM N.A.	[1]
AC	09WD6:	PRELIMINARY;	PRT;	350 AA.	RN	SEQUENCE FROM N.A.
AC	09WD6:	PRELIMINARY;	PRT;	350 AA.	RA	SWINBURNE J., AINSCOUGH R.,
DR	01-NOV-1999 (TREMBlE, 12, Created)				RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DT	01-NOV-1999 (TREMBlE, 12, Last sequence update)				RN	[2]
DT	01-NOV-1999 (TREMBlE, 12, Last annotation update)				RP	SEQUENCE FROM N.A.
DE	WNT8B PROTEIN PRECURSOR.				RX	MEDLINE: 9150718.
GN	WNT8B.				RA	WILSON R., AINSCOUGH R., ANDERSON K., BAINES C., BERKS M., BAINES R., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO R., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER L., LISTER J., MURRAY A., PARSONS J., PERCY C., RIFFEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SUDDON J., TIERRY-MIEC J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMANN P.;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				RA	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans".
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				DR	Nature 368:32-38(1994).
RN	[1]				DR	EMBL: 27021; CAA94227.1; -.
RC	SEQUENCE FROM N.A.				DR	PFAM: PF00110; WNT; 1.
RL	STRAIN=C57BL/6;				DR	PFAM: PF00110; WNT; 1.
RR	RICHARDSON M., REDMOND D., WATSON C., MASON J.O.;				DR	PFAM: PF00110; WNT; 1.
RL	"Mouse Wnt8b is expressed in the developing forebrain and maps to chromosome 19";				DR	PFAM: PF00110; WNT; 1.
CC	Mamm. Genome 0:0-0(1999);				DR	PFAM: PF00110; WNT; 1.
CC	- MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).				DR	PFAM: PF00110; WNT; 1.
CC	- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.				DR	PFAM: PF00110; WNT; 1.
CC	- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.				DR	PFAM: PF00110; WNT; 1.
DR	EMBL: AF13049; AAD31816.1; -.				DR	PFAM: PF00110; WNT; 1.
DR	PROSITE: PS0026; WNT1; 1.				DR	PFAM: PF00110; WNT; 1.
KW	Developmental protein; Glycoprotein.				DR	PFAM: PF00110; WNT; 1.
SO	SEQUENCE 350 AA; 3856 MW; 89442.96 CRC32;				DR	PFAM: PF00110; WNT; 1.
Query Match	32.9 %; Score 875; DB 11; Length 350;				DR	PFAM: PF00110; WNT; 1.
Best Local Similarity	39.8 %; Score 822; DB 5; Length 398;				DR	PFAM: PF00110; WNT; 1.
Matches	125; Conservative 64; Mismatches 94; Indels 12; Gaps 8;				DR	PFAM: PF00110; WNT; 1.
Db	42 VAGAAGSGIEECKYQFWDRWNCPERALQLSHG-GIRSANSNRETAFVHAISAGVMTL 100				DR	PFAM: PF00110; WNT; 1.
Db	62 IGGSGOMGLDECQFOFRNGRWNCSALG-ERTVFGKELVGSREAAFTVATIAGVAHT 120				DR	PFAM: PF00110; WNT; 1.
Db	101 RACSLGLDFDNCGDDSDRNGQLG-GOGNLWGGSDNVFGEAISKQFDALLEGQDARAM 159				DR	PFAM: PF00110; WNT; 1.
Db	121 AACCTGQNLSDCCDKERQGOYHRDEGMWKGGSDADIRYIGKAFVFDAREKONARTLM 180				DR	PFAM: PF00110; WNT; 1.
Qy	160 NHNNNEAGRKAQKGTMKTCKHGVSSECTTCWQWLQPEFEKVGAHLKEKHAALVLDL 219				DR	PFAM: PF00110; WNT; 1.
Qy	181 NHNNNEAGRKAQKGTMKTCKHGVSSECTTCWQWLQPEFEKVGAHLKEKHAALVLDL 240				DR	PFAM: PF00110; WNT; 1.
Db	220 LOGAGNSAAGRGAIAD--TENSISTREWLHEDSPQCLENTLGLTGEGRECLLRGRRA 277				DR	PFAM: PF00110; WNT; 1.
Qy	241 VRASNRKPTFLKIKPLSLYRKPMOTDLYIEKSNSNYCEDPPVGSVGTGRAC--NKT 297				DR	PFAM: PF00110; WNT; 1.
RESULT	13	PRELIMINARY;	PRT;	398 AA.	DR	PFAM: PF00110; WNT; 1.
ID	Q23224:	PRELIMINARY;	PRT;	398 AA.	DR	PFAM: PF00110; WNT; 1.
AC	023224:	PRELIMINARY;	PRT;	398 AA.	DR	PFAM: PF00110; WNT; 1.
DT	01-NOV-1996 (TREMBlE, 01, Created)				DR	PFAM: PF00110; WNT; 1.
DT	01-NOV-1996 (TREMBlE, 01, Last sequence update)				DR	PFAM: PF00110; WNT; 1.
DT	01-NOV-1996 (TREMBlE, 01, Last annotation update)				DR	PFAM: PF00110; WNT; 1.
OY	278 LGRWERRSRRCLGDCGLAVEERRAETVSNSCNCVKHNCVCAVCEQCRRRVTKFC 332				DR	PFAM: PF00110; WNT; 1.
OY	298 -AP-QASGCCDMC--GCGYNTQYARWQNCCKFHNCVYVNCNTCSERTEMTCK 348				DR	PFAM: PF00110; WNT; 1.
RESULT	14	PRELIMINARY;	PRT;	390 AA.	DR	PFAM: PF00110; WNT; 1.
ID	P29753:	PRELIMINARY;	PRT;	390 AA.	DR	PFAM: PF00110; WNT; 1.
AC	P29753:	PRELIMINARY;	PRT;	390 AA.	DR	PFAM: PF00110; WNT; 1.
DT	01-MAY-1997 (TREMBlE, 03, Created)				DR	PFAM: PF00110; WNT; 1.
DT	01-MAY-1997 (TREMBlE, 03, Last sequence update)				DR	PFAM: PF00110; WNT; 1.
DT	01-MAY-1997 (TREMBlE, 03, Last annotation update)				DR	PFAM: PF00110; WNT; 1.
DE	WNT10B.				DR	PFAM: PF00110; WNT; 1.
GN	WNT8D.1 PROTEIN.				DR	PFAM: PF00110; WNT; 1.
OS	Caenorhabditis elegans.				DR	PFAM: PF00110; WNT; 1.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Osteogly1; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidei; Tetradontidae; Fugu.				DR	PFAM: PF00110; WNT; 1.
OC	Rhabdilina; Nematoidea; Rhabditida; Rhabditidae; Peledarinae; Caenorhabditis.				DR	PFAM: PF00110; WNT; 1.
OC	Rhabdilina; Rhabditida; Rhabditidae; Peledarinae; Caenorhabditis.				DR	PFAM: PF00110; WNT; 1.
CC	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.				DR	PFAM: PF00110; WNT; 1.
CC	- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).				DR	PFAM: PF00110; WNT; 1.
CC	- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE				DR	PFAM: PF00110; WNT; 1.

CC -I- EXTRACELLULAR MATRIX; TO OTHER MEMBERS OF THE WNT FAMILY.  
 DR EMBL; AF051616; AAC33899\_1; -.  
 DR PROSITE; PS00246; WNT1; 1.  
 DR PFAM; PF00110; wnt; 1.  
 KW Developmental protein; Glycoprotein.  
 SQ SEQUENCE 390 AA; 43656 MW; B432800B CRC32;  
 Query Match 29.8%; Score 793; DB 13; Length 390;  
 Best Local Similarity 40.3%; Pred. No. 1.59e-179; Mismatches 100; Indexes 33; Gaps 19;  
 Matches 141; Conservative 76; Mismatches 100; Indexes 33; Gaps 19;  
 Db 42 LTPNSVCLKLGLSKRQMRMVCYRSPPDATASALQCIQVALHEQYQYQLQRDQRWNCSSLEG 101  
 | :: :| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 | LGASICCNKIRGLAPRGRACOSRDPATIIVIGEGSOMGCGCFOFQRNGRWCNAL-G-E 89  
 Qy 32 KLPHNHTILNRGPRESAFLSAMLAGVAHSAVASACSMGKLRGGCEAKRQQDDDKIRKL 161  
 | :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 90 R-TVFGKELKGWSREAAFTYATAAGVHAIATRACTQGNLSDGCCD-K----EK----E 137  
 Db 162 TOLQOSIQKDDLSSMOETWENGCSHDWRYGDRFSRDWLDSRGSPRDIHARUKIHNNRY 221  
 Qy 138 -Q-G-Q-YHRDE--G---WKNGGCSADIRYIGFKAQVFVDAIREKONARTMLNHNNEA 187  
 Db 222 GRQIVIDVNMRKCKCHGTSGSCOFQTCWVHSPEFRLGSSLKEFKFLSLILVNSQNKNKV 281  
 | :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 188 GRKILEENNMKLECKCHGVSGCPTKCTWLTQFRELGIVKUOKYNEAWHVEP-VRAS-R 245  
 Db 282 FNPRISSGVSGSTGGLNNGRRRSMSRELYFEKSPDCEPNSUDAGTQGRICNKTSQS 341  
 Qy 246 -NKR-PFLKIKKP-LS-TYRPMTDLVYIENSPNCEDEDPYTGSGTQGRACNKTAPQ 300  
 Db 342 TDSCGSLLCGRGHNTLKTHSERCNCRCRPHCCVYLCEBCCR-L-TEWNVYCK 390  
 Qy :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 301 ASGCDLMCGRGYNTHOYARVWOCNCCKPHWCCIVVKCNITCSERTE-MYICK 349

RESULT 15  
 ID P79856 PRELIMINARY; PRM; 389 AA.  
 AC P79856;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE PWNT-10A.  
 OS Pleurodeles walldii (iberian ribbed newt).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Caudata; Salamandroidea; Pleurodeles.  
 [1] SEQUENCE FROM N.A.  
 RA CAUBIT X., NICOLAS S., SHI D., LE PARCO;  
 RL Dev. Dyn. 0-0(0).  
 CC -I- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).  
 CC SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.  
 CC -I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.  
 DR EMBL; U65428; AA383531\_1; -.  
 DR PROSITE; PS00246; WNT1; 1.  
 DR PFAM; PF00110; wnt; 1.  
 KW Developmental protein; Glycoprotein.  
 SQ SEQUENCE 389 AA; 43972 MW; B534839A CRC32;  
 Query Match 27.6%; Score 734; DB 13; Length 389;  
 Best Local Similarity 41.6%; Pred. No. 4.16e-163; Mismatches 102; Indexes 43; Gaps 16;  
 Matches 148; Conservative 63; Mismatches 102; Indexes 43; Gaps 16;  
 Db 39 LNANTVCLLPGLTEROLEVCMRNPDVTAATGQIQIINHECQHQFKERWNCSSLETKN 98  
 | :| :| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 32 LGASICCNKIRGLAPRGRACOSRDPATIIVIGEGSOMGCGCFOFQRNGRWCNAL-G-E 91

99 KIPYESVVFSGYRESAVYKIAAAGVHAFVSACMSMGKIKACCGCDEKKRGERGFRLKL 158

Search completed: Thu Mar 30 12:44:05 2000  
 Job time : 94 secs.

Qy 92 : : : : : | ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Qy 159 HRLQLEAMRGRGKGMVHGVLHMPSPVGQPOETWEWGCGSPDVIEGERSFDLREMYR 218  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |:  
 Qy 142 HR-----D---E-G---WKNGGCSADIRYIGFKAQVFVDAIREKONARTMLNHNNEA 174  
 Db 219 DIHARMLHNRVGGQVVLDMGRKCKGTSGSQQLKTVQFPRVNLKDFRHG 278  
 Qy | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|:  
 Db 279 ATLIRP-H-NRNTGCV-DGHIPHRRSSINS-LYFEKSPDCEPSEPOLDASAGTOMIC 334  
 Qy | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|:  
 Db 335 NKTSGMDNCESLCGGRGHNILRQTCSRERCKFHWCCVYCEERV-TEWNVYCK 389  
 Qy | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|:  
 295 NKTQAQSGCDLMCGRGYNTHOYARVWOCNCCKPHWCCIVVKCNITCSERTE-MYICK 349

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